

Supplemental Table 2:**Peptides of cellular proteins co-purified by the Strep-NP (vRNP components)**

Band	Acc.	No	Protein	Peptides*	Probability**
1	Q13085		Acetylcarboxylase 1	R.ITSENPDGEFKPSSGTVQELNFR.S	0.9940
1	Q13263		Transcription intermediary factor 1-beta	K.LSPPYSSPQEFAQDVGR.M	0.9682
2	Q16531		DNA damage binding protein 1 DDB1	R.QGQGQLVTC[160]SGAFKEGSLR.I K.LGKDPTNTYFIVGTAM[147]VYPEEAEPK.Q	0.9877 0.9103
2	P09874		Poly[ADP-Ribose]polymerase-1 PARP1	K.C[160]SESIPKDSL.R.M K.AEPVEVVAPR.G K.VVDRDSEEEAIIR.K R.GGSDDSSKDPIDVNYEK.L K.GIYFADM[147]VSK.S K.TLGDFAAEYAK.S K.AM[147]VEYEIDLQKM[147]PLGK.L K.SDAYYC[160]TGDVTAWTK.C R.VVSEDFLQDVSASTK.S R.TTNFAGILSQGLR.I K.NTHATHTHNAVDLEVIDIFKIER.E K.SLQELFLAHILSPWGAEVKAEPVEVVAAPR.G R.TAGQPEGGPAGDFGQSC[160]FPAEAGRDTLSR.T	0.9372 0.9918 0.9684 0.9999 0.9939 0.9882 0.9827 0.9203 0.9945 0.9939 0.9996 0.9794 0.9129
2	Q14694		Ubiquitin carboxyl-terminal hydrolase 10	K.GLSEDTTEETLKESFDGSVR.A R.AIRLELQGPR.G	0.9987 0.9971
3	P19338		Nucleolin (Protein C23)	R.HGNQYIQVNEPWKR.I	0.9993
3	P56192		Methionyl-tRNA synthethase	R.LNQDQLDAVSKYQEVTNNLEFAK.E	0.9955
3	Q9BV09		Membrane component Chromosome 11, surface marker 1	R.SFM[147]ALSQDIQK.T	0.9918
3	P09874		Poly[ADP-Ribose]polymerase-1 PARP1	R.TTNFAGILSQGLR.I	0.9940
4	P13010		ATP-dependent DNA helicase, 80 kDa subunit	R.YGSDIVPFSK.V R.HIEIFTDLSSR.F K.IKTLFPLIEAK.K R.HLM[147]LPDFDLLEDIESK.I K.DKPSGDTAAVFEEGGDVDDLLDM[147]I.-	0.9851 0.9913 0.9875 0.9997 0.9805
4	Q01844		RNA-binding protein EWS (EWS oncogene)	R.GM[147]PPPLRGPGGGPGGGPM[147]GR.M R.QDHPSM[147]GVYQQESGGFSGPGENR.S K-AAVEWFDGKDFQGSK.L	0.9718 0.9995 0.9989
4	Q12906		Interleukin enhancer-bindign factor 3	K.HSSVYPTQEELEAVQNM[147]VSHTER.A	0.9984
5	P08107		Heat shock 70kDa protein 1 (HSP70.1)(HASP70-1/-2)	K.NALESYAFNM[147]K.S R.TTPSYVAFTDER.L R.IINEPTAAAIAYGLDR.T	0.9920 0.9448 0.9554
5	P11142		Heat shock cognate 71kDa protein	K.VQVEYKGETK.T R.STAGDTHLGGEDFDNR.L	0.9666 0.9088

		K.MKEIAEAYLGK.K	0.9219
		K.NQVAM[147]NPTNTVFDAK.R	0.9541
		K.SQIHDIVLVGGSTR.I	0.9895
		R.M[147]VNHFIAEFK.R	0.9939
		K.NSLESYAFNM[147]K.S	0.9851
		R.TTPSYVAFTDTER.L	0.9230
		K.SFYPEEVSSM[147]VLTK.M	0.9588
		R.IINEPTAAAIAYGLDK.K	0.9774
		R.LGSLVDEFKELVYPPDYNPEGK.V	0.9430
		K.KPGGFIDISLFYR.D	0.9323
		R.ILELDQFKGQQGQK.R	0.9997
		R.KEFSPFGTITSAK.V	0.9602
		R.ALDTM[147]NFDVIK.G	0.9863
		R.IVATKPLYVALAQR.K	0.9990
		K.GFGFVC[160]FSSPEEATK.A	0.9298
		K.ITGM[147]LLEIDNSELLHM[147]LESPESLR.S	0.9978
		K.ALYDTFSAGNILSC[160]K.V	0.9783
		R.INEILSNALK.R	0.9823
		R.IFLLGLADNEAAIVQAEESETKER.L	0.9494
		K.KENVATTDTLESTTVGTSV.-	0.9981
		K.LPETNLFETEETRK.I	0.9359
		K.VTYHPDGPEGQAYDVDFTPPFR.R	0.9883
		R.YLDLILNDFVR.Q	0.9889
		K.VTYHPDGPEGQAYDVDFTPPFR.R	0.9883
		R.ELAQQVQQVADDYGK.C	0.9755
5	P12956	ATP-dependent DNA helicase, 70 kDa subunit	
5	P11940	Polyadenylate-binding protein 1 (PABP1)	
5	P52272	Heterogeneous nuclear riboprotein M (hnRNP M)	
5	Q9UHB9	Signal recognition particle 68 kDa protein	
5	Q14046	Lysyl-tRNA synthethase	
5	Q92841	Probable RNA-dependent helicase p72	
6	P04720	Elongation factor 1-alpha1	
6	P11182	Lipoamide acyltransferase component	
6	Q13885	Beta tubulin (Tubulin, beta polypeptide)	
6	Q9Y230	RuvB-like 2	
6	Q13838	Spliceosome RNA helicase BAT1	
6	P05209	Tubulin alpha-1 chain	

6	P05217	Tubulin beta-2 chain	R.LISQIVSSITASLR.F R.ALTVPELTQQM[147]FDSK.N K.GHYTEGAELVDSVLVVVRK.E R.YLTVAAVFR.G R.LHFFM[147]PGFAPLTSR.G R.SGPFGQLFRPDNFVFGQSGAGNNWAK.G K.GHYTEGAELVDSVLVVVRK.K R.ISVYYNEATGGK.Y R.ISEQFTAM[147]FR.R R.AILVDLEPGTM[147]DSVR.S R.ALTVPELTQQM[147]FDSK.N R.YLTVAAVFR.G R.LHFFM[147]PGFAPLTSR.G R.ALTVPELTQQVFDAK.N K.GHYTEGAELVDSVLVVVRK.E R.SGPFGQLFRPDNFVFGQSGAGNNWAK.G K.GHYTEGAELVDSVLVVVRK.K K.M[147]AVTFIGNSTAIQELFK.R	0.9351 0.9939 0.9872 0.9508 0.9535 0.9662 0.9845 0.9941 0.9435 0.9932 0.9917 0.9508 0.9265 0.9888 0.9951 0.9306 0.9848 0.9750
6	P05218	Tubulin beta-5 chain	R.ISEQFTAM[147]FR.R R.AILVDLEPGTM[147]DSVR.S R.YLTVAAVFR.G K.NSSYFVEWIPNNVK.S R.ALTVPELTQQVFDAK.N K.GHYTEGAELVDSVLVVVRK.E R.SGPFGQLFRPDNFVFGQSGAGNNWAK.G K.GHYTEGAELVDSVLVVVRK.K K.M[147]AVTFIGNSTAIQELFK.R	0.9251 0.9813 0.9703 0.9959 0.9933 0.9992 0.9888
7	P05218	Tubulin beta-5 chain	R.ISEQFTAM[147]FR.R R.AILVDLEPGTM[147]DSVR.S R.YLTVAAVFR.G K.NSSYFVEWIPNNVK.S R.ALTVPELTQQVFDAK.N K.GHYTEGAELVDSVLVVVRK.E R.AVFVDLEPTVIDEV.R.T	0.9251 0.9813 0.9703 0.9959 0.9933 0.9992 0.9888
7	P05209	Tubulin alpha-1 chain	K.SYELPDGQVITIGNER.F K.GINSSNVENQLQATQAAR.K R.HGFC[160]GIPITDTGR.M	0.9832 0.9546 0.9972
8	P02570	Actin, cytoplasmatic 1 (Beta Actin)	K.REDLVVAAPAGITLK.E K.ALALGASTVM[147]M[147]GSLLAATTEAPGEYFFSDGIR.L	0.9706 0.9956
8	P52292	Importin Alpha 2	K.LPIVNEDDELVAAIAR.T	0.9772
8	P12268	Inosine-5'-monophosphate dehydrogenase 2	R.SLYASSPAGGVYATR.S R.VEVERDNLNAEDIM[147]R.L R.ISLPLPNFSSLNLR.E	0.9943 0.9769 0.9252
8	P08670	Vimentin	R.M[147]TDQEAIQDLWQWRK.S K.MSVQPTVSLGGFEITPPVVLRLK.C	0.9999 0.9147
9	P06748	Nucleophosmin (NPM)	R.TTTGNKVGALK.G K.GAVDGGLSIPHSTK.R	0.9823 0.9645
10	P46777	60S ribosomal protein L5	K.AIRGHILENNPALEK.L R.GHLENNPALEKLLPHIR.G	0.9977 0.9816
10	P05388	60S acidic ribosomal protein P0	R.NVASVC[160]LQIGYPTVASVPHSIINGYKR.V	0.9306

10	P09651	Heterogeneous nuclear riboprotein A1	K.TSFFQALGITT.K.I R.VLALSvetDyTfPLAEK.V R.SSGPYGGGGQYFAKPR.N	0.9852 0.9831 0.9964
11	P32969	60S ribosomal protein L9	K.FLDGIYVSEK.S R.DFNHINVELSLLGKK.K -.M[147]KTILSNQTVDIPENVDTLK.G K.TILSNQTVDIPENVDTLKGR.T R.VNQAIWLLC[160]TGAR.E K.TIAEC[160]LADELINAAK.G	0.9634 0.9015 0.9936 0.9459 0.9431 0.9669
11	P46782	40S ribosomal protein S5	R.AFGYYGPLR.S R.NPPGFAFVEFEDPRDAADAVR.E	0.9605 0.9971
11	P23152	Splicing factor SFR3		
12	P32969	60S ribosomal protein L9	K.TILSNQTVDIPENVDTLKGR.T	0.9997
12	P46782	40S ribosomal protein S5	R.VNQAIWLLC[160]TGAR.E	0.9067
12	P23821	40S ribosomal protein S7 (S8)	K.LTGKDVNFEFPEM[147]QL.- R.TLTAVHDAILEDLVFPSEIVGKR.I	0.9443 0.9919

* dots after the first and before the last amino acid indicate the site of tryptic digestion, numbers between rectangular brackets show modified molecular weights.

** Peptide probabilities were calculated with Peptide Prophet with a cut off value of 0.9 (Keller et al. 2002, Ref. 22).